

## SEQUENCE LISTING

<110> Kunkel, Andreas  
 Veen, Markus  
 Lang, Christine

<120> Method for producing ergosta-5,7-dienol and/or biosynthetic  
 intermediate and/or secondary products thereof in transgenic  
 organisms

<130> 12810-00126-US

<150> PCT/EP2004/002582

<151> 2004-03-12

<150> DE 103 12 314.8

<151> 2003-03-19

<160> 14

<170> PatentIn version 3.3

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<212> DNA

<213> Saccharomyces cerevisiae

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Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr	
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aag gct aag tgg gca tcc ggt cca ctt tca tgt gtt tct att ttc cat	336
Lys Ala Lys Trp Ala Ser Gly Pro Leu Ser Cys Val Ser Ile Phe His	
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Lys Phe Val Val Ile Ala Ser Thr Arg Asp Leu Ala Arg Lys Ile Leu	
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Ile Leu Arg Pro Cys Asn Trp Val Phe Leu Asp Gly Lys Ala His Thr	
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gat tac aga aaa tca tta aac ggt ctt ttc act aaa caa gct ttg gct	528
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Tyr Leu Val Thr Ala Ala Leu Glu Leu Val Asn Phe Pro Ile Ile Ile	
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Pro Tyr Thr Lys Thr Trp Tyr Gly Lys Lys Thr Ala Asp Met Ala Met	
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Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe	
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Tyr Val Met Ile Thr Phe Ala Ala Leu Leu Gly Lys Phe Ala Leu Tyr	
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Phe Ala Thr Leu Ile Cys Ile Leu Leu Val Trp Asp Gln Val Ala Tyr  
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Gln Ile Lys Lys Gly Ser Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro  
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Ile Ile Gly Pro Phe Leu Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr  
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Lys Phe Val Val Ile Ala Ser Thr Arg Asp Leu Ala Arg Lys Ile Leu  
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Gln Ser Ser Lys Phe Val Lys Pro Cys Val Val Asp Val Ala Val Lys  
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Gly Gly Lys Pro Val Cys Val Met Asp Ala Trp Cys Lys Leu Met His  
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Asp Ala Lys Asn Ser Asn Asp Asp Asp Ser Arg Ile Tyr His Arg Glu  
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Tyr Pro Ala Leu His Asp Pro Glu Val Tyr Glu Asn Pro Asp Glu Phe  
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 Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser  
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act acg aga gcg gtt gcg gta cgt agg aag gct ctt tca att ttg gca Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala 115 120 125			384
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cct ttg ccc gtt ggt gtt ata ggc ccc ttg gtt atc gat ggt aca tct Pro Leu Pro Val Gly Val Ile Gly Pro Leu Val Ile Asp Gly Thr Ser 165 170 175			528
tat cat ata cca atg gca act aca gag ggt tgt ttg gta gct tct gcc Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala 180 185 190			576
atg cgt ggc tgt aag gca atc aat gct ggc ggt ggt gca aca act gtt Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr Val 195 200 205			624
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gaa agt tcc aac tgt ata aca ttg atg aaa gaa gtg gac ggt gat ttg Glu Ser Ser Asn Cys Ile Thr Leu Met Lys Glu Val Asp Gly Asp Leu 405 410 415	1248
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Ser Gly Ser Lys Val Lys Ser Leu Ser Ser Ala Gln Ser Ser Ser Ser  
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Gly Pro Ser Ser Ser Ser Glu Glu Asp Asp Ser Arg Asp Ile Glu Ser  
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Leu Asp Lys Lys Ile Arg Pro Leu Glu Glu Leu Glu Ala Leu Leu Ser  
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Ser Gly Asn Thr Lys Gln Leu Lys Asn Lys Glu Val Ala Ala Leu Val  
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Ile His Gly Lys Leu Pro Leu Tyr Ala Leu Glu Lys Lys Leu Gly Asp  
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Thr Thr Arg Ala Val Ala Val Arg Arg Lys Ala Leu Ser Ile Leu Ala  
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Tyr His Ile Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Ala  
 180 185 190

Met Arg Gly Cys Lys Ala Ile Asn Ala Gly Gly Gly Ala Thr Thr Val  
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Leu Thr Lys Asp Gly Met Thr Arg Gly Pro Val Val Arg Phe Pro Thr  
 210 215 220

Leu Lys Arg Ser Gly Ala Cys Lys Ile Trp Leu Asp Ser Glu Glu Gly  
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Gln Asn Ala Ile Lys Lys Ala Phe Asn Ser Thr Ser Arg Phe Ala Arg  
 245 250 255

Leu Gln His Ile Gln Thr Cys Leu Ala Gly Asp Leu Leu Phe Met Arg  
 260 265 270

Phe Arg Thr Thr Thr Gly Asp Ala Met Gly Met Asn Met Ile Ser Lys  
 275 280 285

Gly Val Glu Tyr Ser Leu Lys Gln Met Val Glu Glu Tyr Gly Trp Glu  
 290 295 300

Asp Met Glu Val Val Ser Val Ser Gly Asn Tyr Cys Thr Asp Lys Lys  
 305 310 315 320

Pro Ala Ala Ile Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Ala  
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Glu Ala Thr Ile Pro Gly Asp Val Val Arg Lys Val Leu Lys Ser Asp  
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Val Ser Ala Leu Val Glu Leu Asn Ile Ala Lys Asn Leu Val Gly Ser  
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Val Thr Ala Val Phe Leu Ala Leu Gly Gln Asp Pro Ala Gln Asn Val

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 Arg Ile Ser Val Ser Met Pro Ser Ile Glu Val Gly Thr Ile Gly Gly  
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 Gly Thr Val Leu Glu Pro Gln Gly Ala Met Leu Asp Leu Leu Gly Val  
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 Arg Gly Pro His Ala Thr Ala Pro Gly Thr Asn Ala Arg Gln Leu Ala  
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 Arg Ile Val Ala Cys Ala Val Leu Ala Gly Glu Leu Ser Leu Cys Ala  
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 Ala Leu Ala Ala Gly His Leu Val Gln Ser His Met Thr His Asn Arg  
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 Lys Pro Ala Glu Pro Thr Lys Pro Asn Asn Leu Asp Ala Thr Asp Ile  
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 att ggt tta agt cat ttc ttg gct tta cca ttg gcc caa aga atc tct                      96  
 Ile Gly Leu Ser His Phe Leu Ala Leu Pro Leu Ala Gln Arg Ile Ser  
                          20                      25                      30  
 ttg atc ata ata att cct ttc att tac aat att gta tgg caa tta cta                      144  
 Leu Ile Ile Ile Ile Pro Phe Ile Tyr Asn Ile Val Trp Gln Leu Leu  
                          35                      40                      45

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Trp	Val	Gly	Ser	Ala	Val	Val	Tyr	Gly	Met	Lys	Pro	Tyr	Glu	Phe	Phe	
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gaa	gaa	tgt	caa	aag	aaa	tac	ggt	gat	att	ttt	tca	ttc	ggt	ttg	tta	288
Glu	Glu	Cys	Gln	Lys	Lys	Tyr	Gly	Asp	Ile	Phe	Ser	Phe	Val	Leu	Leu	
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gga	aga	gtc	atg	act	gtg	tat	tta	gga	cca	aag	ggt	cac	gaa	ttt	gtc	336
Gly	Arg	Val	Met	Thr	Val	Tyr	Leu	Gly	Pro	Lys	Gly	His	Glu	Phe	Val	
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Phe	Asn	Ala	Lys	Leu	Ala	Asp	Val	Ser	Ala	Glu	Ala	Ala	Tyr	Ala	His	
	115						120					125				
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Leu	Thr	Thr	Pro	Val	Phe	Gly	Lys	Gly	Val	Ile	Tyr	Asp	Cys	Pro	Asn	
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Ser	Arg	Leu	Met	Glu	Gln	Lys	Lys	Phe	Val	Lys	Gly	Ala	Leu	Thr	Lys	
145					150					155					160	
gaa	gcc	ttc	aag	agc	tac	gtt	cca	ttg	att	gct	gaa	gaa	gtg	tac	aag	528
Glu	Ala	Phe	Lys	Ser	Tyr	Val	Pro	Leu	Ile	Ala	Glu	Glu	Val	Tyr	Lys	
				165					170					175		
tac	ttc	aga	gac	tcc	aaa	aac	ttc	cgt	ttg	aat	gaa	aga	act	act	ggt	576
Tyr	Phe	Arg	Asp	Ser	Lys	Asn	Phe	Arg	Leu	Asn	Glu	Arg	Thr	Thr	Gly	
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Thr	Ile	Asp	Val	Met	Val	Thr	Gln	Pro	Glu	Met	Thr	Ile	Phe	Thr	Ala	
		195					200					205				
tca	aga	tca	tta	ttg	ggt	aag	gaa	atg	aga	gca	aaa	ttg	gat	acc	gat	672
Ser	Arg	Ser	Leu	Leu	Gly	Lys	Glu	Met	Arg	Ala	Lys	Leu	Asp	Thr	Asp	
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Phe	Ala	Tyr	Leu	Tyr	Ser	Asp	Leu	Asp	Lys	Gly	Phe	Thr	Pro	Ile	Asn	
225					230					235					240	
ttc	gtc	ttc	cct	aac	tta	cca	ttg	gaa	cac	tat	aga	aag	aga	gat	cac	768
Phe	Val	Phe	Pro	Asn	Leu	Pro	Leu	Glu	His	Tyr	Arg	Lys	Arg	Asp	His	
			245						250					255		
gct	caa	aag	gct	atc	tcc	ggt	act	tac	atg	tct	ttg	att	aag	gaa	aga	816
Ala	Gln	Lys	Ala	Ile	Ser	Gly	Thr	Tyr	Met	Ser	Leu	Ile	Lys	Glu	Arg	
			260					265					270			
aga	aag	aac	aac	gac	att	caa	gac	aga	gat	ttg	atc	gat	tcc	ttg	atg	864

Arg	Lys	Asn	Asn	Asp	Ile	Gln	Asp	Arg	Asp	Leu	Ile	Asp	Ser	Leu	Met	
		275					280					285				
aag	aac	tct	acc	tac	aag	gat	ggt	gtg	aag	atg	act	gat	caa	gaa	atc	912
Lys	Asn	Ser	Thr	Tyr	Lys	Asp	Gly	Val	Lys	Met	Thr	Asp	Gln	Glu	Ile	
	290					295					300					
gct	aac	ttg	tta	att	ggt	gtc	tta	atg	ggt	ggt	caa	cat	act	tct	gct	960
Ala	Asn	Leu	Leu	Ile	Gly	Val	Leu	Met	Gly	Gly	Gln	His	Thr	Ser	Ala	
305					310					315					320	
gcc	act	tct	gct	tgg	att	ttg	ttg	cac	ttg	gct	gaa	aga	cca	gat	gtc	1008
Ala	Thr	Ser	Ala	Trp	Ile	Leu	Leu	His	Leu	Ala	Glu	Arg	Pro	Asp	Val	
				325					330					335		
caa	caa	gaa	ttg	tac	gaa	gaa	caa	atg	cgt	gtt	ttg	gat	ggt	ggt	aag	1056
Gln	Gln	Glu	Leu	Tyr	Glu	Glu	Gln	Met	Arg	Val	Leu	Asp	Gly	Gly	Lys	
			340					345					350			
aag	gaa	ttg	acc	tac	gat	tta	tta	caa	gaa	atg	cca	ttg	ttg	aac	caa	1104
Lys	Glu	Leu	Thr	Tyr	Asp	Leu	Leu	Gln	Glu	Met	Pro	Leu	Leu	Asn	Gln	
		355					360					365				
act	att	aag	gaa	act	cta	aga	atg	cac	cat	cca	ttg	cac	tct	ttg	ttc	1152
Thr	Ile	Lys	Glu	Thr	Leu	Arg	Met	His	His	Pro	Leu	His	Ser	Leu	Phe	
	370					375					380					
cgt	aag	gtt	atg	aaa	gat	atg	cac	gtt	cca	aac	act	tct	tat	gtc	atc	1200
Arg	Lys	Val	Met	Lys	Asp	Met	His	Val	Pro	Asn	Thr	Ser	Tyr	Val	Ile	
385					390					395					400	
cca	gca	ggt	tat	cac	gtt	ttg	gtt	tct	cca	ggt	tac	act	cat	tta	aga	1248
Pro	Ala	Gly	Tyr	His	Val	Leu	Val	Ser	Pro	Gly	Tyr	Thr	His	Leu	Arg	
				405					410					415		
gac	gaa	tac	ttc	cct	aat	gct	cac	caa	ttc	aac	att	cac	cgt	tgg	aac	1296
Asp	Glu	Tyr	Phe	Pro	Asn	Ala	His	Gln	Phe	Asn	Ile	His	Arg	Trp	Asn	
			420					425					430			
aaa	gat	tct	gcc	tcc	tct	tat	tcc	gtc	ggt	gaa	gaa	gtc	gat	tac	ggt	1344
Lys	Asp	Ser	Ala	Ser	Ser	Tyr	Ser	Val	Gly	Glu	Glu	Val	Asp	Tyr	Gly	
		435					440					445				
ttc	ggt	gcc	att	tct	aag	ggt	gtc	agc	tct	cca	tac	tta	cct	ttc	ggt	1392
Phe	Gly	Ala	Ile	Ser	Lys	Gly	Val	Ser	Ser	Pro	Tyr	Leu	Pro	Phe	Gly	
	450					455					460					
ggt	ggt	aga	cac	aga	tgt	atc	ggt	gaa	cac	ttt	gct	tac	tgt	cag	cta	1440
Gly	Gly	Arg	His	Arg	Cys	Ile	Gly	Glu	His	Phe	Ala	Tyr	Cys	Gln	Leu	
465					470					475					480	
ggt	gtt	cta	atg	tcc	att	ttt	atc	aga	aca	tta	aaa	tgg	cat	tac	cca	1488
Gly	Val	Leu	Met	Ser	Ile	Phe	Ile	Arg	Thr	Leu	Lys	Trp	His	Tyr	Pro	
				485					490					495		
gag	ggt	aag	acc	gtt	cca	cct	cct	gac	ttt	aca	tct	atg	gtt	act	ctt	1536
Glu	Gly	Lys	Thr	Val	Pro	Pro	Pro	Asp	Phe	Thr	Ser	Met	Val	Thr	Leu	

500	505	510	
cca acc ggt cca gcc aag atc atc tgg gaa aag aga aat cca gaa caa			1584
Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln			
515	520	525	
aag atc taa			1593
Lys Ile			
530			
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Ile Gly Leu Ser His Phe Leu Ala Leu Pro Leu Ala Gln Arg Ile Ser			
	20	25	30
Leu Ile Ile Ile Ile Pro Phe Ile Tyr Asn Ile Val Trp Gln Leu Leu			
	35	40	45
Tyr Ser Leu Arg Lys Asp Arg Pro Pro Leu Val Phe Tyr Trp Ile Pro			
	50	55	60
Trp Val Gly Ser Ala Val Val Tyr Gly Met Lys Pro Tyr Glu Phe Phe			
65	70	75	80
Glu Glu Cys Gln Lys Lys Tyr Gly Asp Ile Phe Ser Phe Val Leu Leu			
	85	90	95
Gly Arg Val Met Thr Val Tyr Leu Gly Pro Lys Gly His Glu Phe Val			
	100	105	110
Phe Asn Ala Lys Leu Ala Asp Val Ser Ala Glu Ala Ala Tyr Ala His			
	115	120	125
Leu Thr Thr Pro Val Phe Gly Lys Gly Val Ile Tyr Asp Cys Pro Asn			
	130	135	140
Ser Arg Leu Met Glu Gln Lys Lys Phe Val Lys Gly Ala Leu Thr Lys			
145	150	155	160

Glu Ala Phe Lys Ser Tyr Val Pro Leu Ile Ala Glu Glu Val Tyr Lys  
 165 170 175

Tyr Phe Arg Asp Ser Lys Asn Phe Arg Leu Asn Glu Arg Thr Thr Gly  
 180 185 190

Thr Ile Asp Val Met Val Thr Gln Pro Glu Met Thr Ile Phe Thr Ala  
 195 200 205

Ser Arg Ser Leu Leu Gly Lys Glu Met Arg Ala Lys Leu Asp Thr Asp  
 210 215 220

Phe Ala Tyr Leu Tyr Ser Asp Leu Asp Lys Gly Phe Thr Pro Ile Asn  
 225 230 235 240

Phe Val Phe Pro Asn Leu Pro Leu Glu His Tyr Arg Lys Arg Asp His  
 245 250 255

Ala Gln Lys Ala Ile Ser Gly Thr Tyr Met Ser Leu Ile Lys Glu Arg  
 260 265 270

Arg Lys Asn Asn Asp Ile Gln Asp Arg Asp Leu Ile Asp Ser Leu Met  
 275 280 285

Lys Asn Ser Thr Tyr Lys Asp Gly Val Lys Met Thr Asp Gln Glu Ile  
 290 295 300

Ala Asn Leu Leu Ile Gly Val Leu Met Gly Gly Gln His Thr Ser Ala  
 305 310 315 320

Ala Thr Ser Ala Trp Ile Leu Leu His Leu Ala Glu Arg Pro Asp Val  
 325 330 335

Gln Gln Glu Leu Tyr Glu Glu Gln Met Arg Val Leu Asp Gly Gly Lys  
 340 345 350

Lys Glu Leu Thr Tyr Asp Leu Leu Gln Glu Met Pro Leu Leu Asn Gln  
 355 360 365

Thr Ile Lys Glu Thr Leu Arg Met His His Pro Leu His Ser Leu Phe  
 370 375 380

Arg Lys Val Met Lys Asp Met His Val Pro Asn Thr Ser Tyr Val Ile  
385 390 395 400

Pro Ala Gly Tyr His Val Leu Val Ser Pro Gly Tyr Thr His Leu Arg  
405 410 415

Asp Glu Tyr Phe Pro Asn Ala His Gln Phe Asn Ile His Arg Trp Asn  
420 425 430

Lys Asp Ser Ala Ser Ser Tyr Ser Val Gly Glu Glu Val Asp Tyr Gly  
435 440 445

Phe Gly Ala Ile Ser Lys Gly Val Ser Ser Pro Tyr Leu Pro Phe Gly  
450 455 460

Gly Gly Arg His Arg Cys Ile Gly Glu His Phe Ala Tyr Cys Gln Leu  
465 470 475 480

Gly Val Leu Met Ser Ile Phe Ile Arg Thr Leu Lys Trp His Tyr Pro  
485 490 495

Glu Gly Lys Thr Val Pro Pro Pro Asp Phe Thr Ser Met Val Thr Leu  
500 505 510

Pro Thr Gly Pro Ala Lys Ile Ile Trp Glu Lys Arg Asn Pro Glu Gln  
515 520 525

Lys Ile  
530

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<211> 1491  
<212> DNA  
<213> *Saccharomyces cerevisiae*

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Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr  
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att acc tac gat gcg att gtc atc ggt gct ggt gtt atc ggt cca tgt 96  
Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys  
20 25 30



ggt gct act ggt cta gca aga aag ggt aag aaa gtt ctt atc gta gaa	144
Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu	
35 40 45	
cgt gac tgg gct atg cct gat aga att gtt ggt gaa ttg atg caa cca	192
Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro	
50 55 60	
ggt ggt gtt aga gca ttg aga agt ctg ggt atg att caa tct atc aac	240
Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn	
65 70 75 80	
aac atc gaa gca tat cct gtt acc ggt tat acc gtc ttt ttc aac ggc	288
Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly	
85 90 95	
gaa caa gtt gat att cca tac cct tac aag gcc gat atc cct aaa gtt	336
Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val	
100 105 110	
gaa aaa ttg aag gac ttg gtc aaa gat ggt aat gac aag gtc ttg gaa	384
Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu	
115 120 125	
gac agc act att cac atc aag gat tac gaa gat gat gaa aga gaa agg	432
Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Glu Arg Glu Arg	
130 135 140	
ggt gtt gct ttt gtt cat ggt aga ttc ttg aac aac ttg aga aac att	480
Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile	
145 150 155 160	
act gct caa gag cca aat gtt act aga gtg caa ggt aac tgt att gag	528
Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu	
165 170 175	
ata ttg aag gat gaa aag aat gag gtt gtt ggt gcc aag gtt gac att	576
Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile	
180 185 190	
gat ggc cgt ggc aag gtg gaa ttc aaa gcc cac ttg aca ttt atc tgt	624
Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys	
195 200 205	
gac ggt atc ttt tca cgt ttc aga aag gaa ttg cac cca gac cat gtt	672
Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val	
210 215 220	
cca act gtc ggt tct tcg ttt gtc ggt atg tct ttg ttc aat gct aag	720
Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys	
225 230 235 240	
aat cct gct cct atg cac ggt cac gtt att ctt ggt agt gat cat atg	768
Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met	
245 250 255	

cca atc ttg gtt tac caa atc agt cca gaa gaa aca aga atc ctt tgt	816
Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys	
260 265 270	
gct tac aac tct cca aag gtc cca gct gat atc aag agt tgg atg att	864
Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile	
275 280 285	
aag gat gtc caa cct ttc att cca aag agt cta cgt cct tca ttt gat	912
Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp	
290 295 300	
gaa gcc gtc agc caa ggt aaa ttt aga gct atg cca aac tcc tac ttg	960
Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu	
305 310 315 320	
cca gct aga caa aac gac gtc act ggt atg tgt gtt atc ggt gac gct	1008
Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala	
325 330 335	
cta aat atg aga cat cca ttg act ggt ggt ggt atg act gtc ggt ttg	1056
Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu	
340 345 350	
cat gat gtt gtc ttg ttg att aag aaa ata ggt gac cta gac ttc agc	1104
His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser	
355 360 365	
gac cgt gaa aag gtt ttg gat gaa tta cta gac tac cat ttc gaa aga	1152
Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg	
370 375 380	
aag agt tac gat tcc gtt att aac gtt ttg tca gtg gct ttg tat tct	1200
Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser	
385 390 395 400	
ttg ttc gct gct gac agc gat aac ttg aag gca tta caa aaa ggt tgt	1248
Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys	
405 410 415	
ttc aaa tat ttc caa aga ggt ggc gat tgt gtc aac aaa ccc gtt gaa	1296
Phe Lys Tyr Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu	
420 425 430	
ttt ctg tct ggt gtc ttg cca aag cct ttg caa ttg acc agg gtt ttc	1344
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe	
435 440 445	
ttc gct gtc gct ttt tac acc att tac ttg aac atg gaa gaa cgt ggt	1392
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly	
450 455 460	
ttc ttg gga tta cca atg gct tta ttg gaa ggt att atg att ttg atc	1440
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile	
465 470 475 480	
aca gct att aga gta ttc acc cca ttt ttg ttt ggt gag ttg att ggt	1488

Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly  
 485 490 495

taa

1491

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 <211> 496  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

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Met Ser Ala Val Asn Val Ala Pro Glu Leu Ile Asn Ala Asp Asn Thr  
 1 5 10 15

Ile Thr Tyr Asp Ala Ile Val Ile Gly Ala Gly Val Ile Gly Pro Cys  
 20 25 30

Val Ala Thr Gly Leu Ala Arg Lys Gly Lys Lys Val Leu Ile Val Glu  
 35 40 45

Arg Asp Trp Ala Met Pro Asp Arg Ile Val Gly Glu Leu Met Gln Pro  
 50 55 60

Gly Gly Val Arg Ala Leu Arg Ser Leu Gly Met Ile Gln Ser Ile Asn  
 65 70 75 80

Asn Ile Glu Ala Tyr Pro Val Thr Gly Tyr Thr Val Phe Phe Asn Gly  
 85 90 95

Glu Gln Val Asp Ile Pro Tyr Pro Tyr Lys Ala Asp Ile Pro Lys Val  
 100 105 110

Glu Lys Leu Lys Asp Leu Val Lys Asp Gly Asn Asp Lys Val Leu Glu  
 115 120 125

Asp Ser Thr Ile His Ile Lys Asp Tyr Glu Asp Asp Glu Arg Glu Arg  
 130 135 140

Gly Val Ala Phe Val His Gly Arg Phe Leu Asn Asn Leu Arg Asn Ile  
 145 150 155 160

Thr Ala Gln Glu Pro Asn Val Thr Arg Val Gln Gly Asn Cys Ile Glu  
 165 170 175

Ile Leu Lys Asp Glu Lys Asn Glu Val Val Gly Ala Lys Val Asp Ile  
 180 185 190

Asp Gly Arg Gly Lys Val Glu Phe Lys Ala His Leu Thr Phe Ile Cys  
 195 200 205

Asp Gly Ile Phe Ser Arg Phe Arg Lys Glu Leu His Pro Asp His Val  
 210 215 220

Pro Thr Val Gly Ser Ser Phe Val Gly Met Ser Leu Phe Asn Ala Lys  
 225 230 235 240

Asn Pro Ala Pro Met His Gly His Val Ile Leu Gly Ser Asp His Met  
 245 250 255

Pro Ile Leu Val Tyr Gln Ile Ser Pro Glu Glu Thr Arg Ile Leu Cys  
 260 265 270

Ala Tyr Asn Ser Pro Lys Val Pro Ala Asp Ile Lys Ser Trp Met Ile  
 275 280 285

Lys Asp Val Gln Pro Phe Ile Pro Lys Ser Leu Arg Pro Ser Phe Asp  
 290 295 300

Glu Ala Val Ser Gln Gly Lys Phe Arg Ala Met Pro Asn Ser Tyr Leu  
 305 310 315 320

Pro Ala Arg Gln Asn Asp Val Thr Gly Met Cys Val Ile Gly Asp Ala  
 325 330 335

Leu Asn Met Arg His Pro Leu Thr Gly Gly Gly Met Thr Val Gly Leu  
 340 345 350

His Asp Val Val Leu Leu Ile Lys Lys Ile Gly Asp Leu Asp Phe Ser  
 355 360 365

Asp Arg Glu Lys Val Leu Asp Glu Leu Leu Asp Tyr His Phe Glu Arg  
 370 375 380

Lys Ser Tyr Asp Ser Val Ile Asn Val Leu Ser Val Ala Leu Tyr Ser  
 385 390 395 400

Leu Phe Ala Ala Asp Ser Asp Asn Leu Lys Ala Leu Gln Lys Gly Cys

	405		410		415
Phe Lys Tyr	Phe Gln Arg Gly Gly Asp Cys Val Asn Lys Pro Val Glu				
	420		425		430
Phe Leu Ser Gly Val Leu Pro Lys Pro Leu Gln Leu Thr Arg Val Phe					
	435		440		445
Phe Ala Val Ala Phe Tyr Thr Ile Tyr Leu Asn Met Glu Glu Arg Gly					
	450		455		460
Phe Leu Gly Leu Pro Met Ala Leu Leu Glu Gly Ile Met Ile Leu Ile					
	465		470		475
					480
Thr Ala Ile Arg Val Phe Thr Pro Phe Leu Phe Gly Glu Leu Ile Gly					
	485		490		495

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 <212> DNA  
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gct ttg aag ctg aag ttt tgc aga aca ccg cta ttc tcc atc tat gat	96
Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp	
20 25 30	
cag tcc acg tct cca tat ctc ttg cac tgt ttc gaa ctg ttg aac ttg	144
Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu	
35 40 45	
acc tcc aga tcg ttt gct gct gtg atc aga gag ctg cat cca gaa ttg	192
Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu	
50 55 60	
aga aac tgt gtt act ctc ttt tat ttg att tta agg gct ttg gat acc	240
Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr	
65 70 75 80	
atc gaa gac gat atg tcc atc gaa cac gat ttg aaa att gac ttg ttg	288
Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu	
85 90 95	

cgt cac ttc cac gag aaa ttg ttg tta act aaa tgg agt ttc gac gga Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly 100 105 110	336
aat gcc ccc gat gtg aag gac aga gcc gtt ttg aca gat ttc gaa tcg Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser 115 120 125	384
att ctt att gaa ttc cac aaa ttg aaa cca gaa tat caa gaa gtc atc Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile 130 135 140	432
aag gag atc acc gag aaa atg ggt aat ggt atg gcc gac tac atc tta Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu 145 150 155 160	480
gat gaa aat tac aac ttg aat ggg ttg caa acc gtc cac gac tac gac Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp 165 170 175	528
gtg tac tgt cac tac gta gct ggt ttg gtc ggt gat ggt ttg acc cgt Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg 180 185 190	576
ttg att gtc att gcc aag ttt gcc aac gaa tct ttg tat tct aat gag Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu 195 200 205	624
caa ttg tat gaa agc atg ggt ctt ttc cta caa aaa acc aac atc atc Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile 210 215 220	672
aga gat tac aat gaa gat ttg gtc gat ggt aga tcc ttc tgg ccc aag Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys 225 230 235 240	720
gaa atc tgg tca caa tac gct cct cag ttg aag gac ttc atg aaa cct Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro 245 250 255	768
gaa aac gaa caa ctg ggg ttg gac tgt ata aac cac ctc gtc tta aac Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn 260 265 270	816
gca ttg agt cat gtt atc gat gtg ttg act tat ttg gcc ggt atc cac Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His 275 280 285	864
gag caa tcc act ttc caa ttt tgt gcc att ccc caa gtt atg gcc att Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile 290 295 300	912
gca acc ttg gct ttg gta ttc aac aac cgt gaa gtg cta cat ggc aat Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn 305 310 315 320	960
gta aag att cgt aag ggt act acc tgc tat tta att ttg aaa tca agg	1008

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg  
 325 330 335  
 act ttg cgt ggc tgt gtc gag att ttt gac tat tac tta cgt gat atc 1056  
 Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile  
 340 345 350  
 aaa tct aaa ttg gct gtg caa gat cca aat ttc tta aaa ttg aac att 1104  
 Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile  
 355 360 365  
 caa atc tcc aag atc gaa cag ttt atg gaa gaa atg tac cag gat aaa 1152  
 Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys  
 370 375 380  
 tta cct cct aac gtg aag cca aat gaa act cca att ttc ttg aaa gtt 1200  
 Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val  
 385 390 395 400  
 aaa gaa aga tcc aga tac gat gat gaa ttg gtt cca acc caa caa gaa 1248  
 Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu  
 405 410 415  
 gaa gag tac aag ttc aat atg gtt tta tct atc atc ttg tcc gtt ctt 1296  
 Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu  
 420 425 430  
 ctt ggg ttt tat tat ata tac act tta cac aga gcg tga 1335  
 Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala  
 435 440

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 <211> 444  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

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Met Gly Lys Leu Leu Gln Leu Ala Leu His Pro Val Glu Met Lys Ala  
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Ala Leu Lys Leu Lys Phe Cys Arg Thr Pro Leu Phe Ser Ile Tyr Asp  
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Gln Ser Thr Ser Pro Tyr Leu Leu His Cys Phe Glu Leu Leu Asn Leu  
 35 40 45

Thr Ser Arg Ser Phe Ala Ala Val Ile Arg Glu Leu His Pro Glu Leu  
 50 55 60

Arg Asn Cys Val Thr Leu Phe Tyr Leu Ile Leu Arg Ala Leu Asp Thr  
 65 70 75 80

Ile Glu Asp Asp Met Ser Ile Glu His Asp Leu Lys Ile Asp Leu Leu  
85 90 95

Arg His Phe His Glu Lys Leu Leu Leu Thr Lys Trp Ser Phe Asp Gly  
100 105 110

Asn Ala Pro Asp Val Lys Asp Arg Ala Val Leu Thr Asp Phe Glu Ser  
115 120 125

Ile Leu Ile Glu Phe His Lys Leu Lys Pro Glu Tyr Gln Glu Val Ile  
130 135 140

Lys Glu Ile Thr Glu Lys Met Gly Asn Gly Met Ala Asp Tyr Ile Leu  
145 150 155 160

Asp Glu Asn Tyr Asn Leu Asn Gly Leu Gln Thr Val His Asp Tyr Asp  
165 170 175

Val Tyr Cys His Tyr Val Ala Gly Leu Val Gly Asp Gly Leu Thr Arg  
180 185 190

Leu Ile Val Ile Ala Lys Phe Ala Asn Glu Ser Leu Tyr Ser Asn Glu  
195 200 205

Gln Leu Tyr Glu Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile  
210 215 220

Arg Asp Tyr Asn Glu Asp Leu Val Asp Gly Arg Ser Phe Trp Pro Lys  
225 230 235 240

Glu Ile Trp Ser Gln Tyr Ala Pro Gln Leu Lys Asp Phe Met Lys Pro  
245 250 255

Glu Asn Glu Gln Leu Gly Leu Asp Cys Ile Asn His Leu Val Leu Asn  
260 265 270

Ala Leu Ser His Val Ile Asp Val Leu Thr Tyr Leu Ala Gly Ile His  
275 280 285

Glu Gln Ser Thr Phe Gln Phe Cys Ala Ile Pro Gln Val Met Ala Ile  
290 295 300



Ala Thr Leu Ala Leu Val Phe Asn Asn Arg Glu Val Leu His Gly Asn  
 305 310 315 320

Val Lys Ile Arg Lys Gly Thr Thr Cys Tyr Leu Ile Leu Lys Ser Arg  
 325 330 335

Thr Leu Arg Gly Cys Val Glu Ile Phe Asp Tyr Tyr Leu Arg Asp Ile  
 340 345 350

Lys Ser Lys Leu Ala Val Gln Asp Pro Asn Phe Leu Lys Leu Asn Ile  
 355 360 365

Gln Ile Ser Lys Ile Glu Gln Phe Met Glu Glu Met Tyr Gln Asp Lys  
 370 375 380

Leu Pro Pro Asn Val Lys Pro Asn Glu Thr Pro Ile Phe Leu Lys Val  
 385 390 395 400

Lys Glu Arg Ser Arg Tyr Asp Asp Glu Leu Val Pro Thr Gln Gln Glu  
 405 410 415

Glu Glu Tyr Lys Phe Asn Met Val Leu Ser Ile Ile Leu Ser Val Leu  
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Leu Gly Phe Tyr Tyr Ile Tyr Thr Leu His Arg Ala  
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35

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32

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62